SEQUENCE LISTING

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<110> Galloway, Susan May
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           Davis, George Henry
          Gregan, Scott Michael
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           Hanrahan, James Patrick
           Juengel, Jennifer Lee
           McNatty, Kenneth Pattrick
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           Mulsant, Philippe
           Powell, Richard Patrick
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15	Thr	Trp	Ser	Leu -270	Leu	Asn	His	Leu	Gly -265	Gly	Arg	His	Arg	Pro -260	Gly
20	Leu	Leu	Ser	Pro -255	Leu	Leu	Glu	Val	Leu -250	Tyr	Asp	Gly	His	Gly -245	Glu
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	His	Lys	Arg -90	Asn	Ile	His	Met	Ser -85	Val	Asn	Phe	Thr	-80	Ата	GIU	Asp
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                                     -310
                -315
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                                     -295
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     Arg Leu Tyr Lys Ala Tyr Ala Thr Lys Glu Gly Thr Pro Lys
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                                     -220
                 -225
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9 9 1

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-305

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-310

-315

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WO 03/102199



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<223> c to t at 83 in [787] sheep changing tct serine codon to ttt phenylalanine

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 Asp Cys Pro Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr 20
- atg gtg cag aac atc atc cat gag aaa ctt gac tcc tca gtg cca aga 144
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25
     ctttcatttt tccttgccct atcctttgtg gtagtggagc ctggatgctg ttacccatgt
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     aaaaggaaag gtttaaagcg ttatcctttg ggcttttatc agaacatgtt gctgaacacc
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30
     aagcttttca ag atg gtc ctc ctg agc atc ctt aga atc ctt ctt tgg gga
     291
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                   1
                                    5
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35
     ctq qtq ctt ttt atq gaa cat agg gtc caa atg aca cag gta ggg cag
     339
     Leu Val Leu Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln
         15
                              20
                                                  25
40
     ccc tct att qcc cac ctq cct gag gcc cct acc ttg ccc ctg att cag
     387
     Pro Ser Ile Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln
                                                                   45
                          35
                                              40
     30
45
     gag ctg cta gaa gaa gcc cct ggc aag cag cag agg aag ccg cgg gtc
     435
     Glu Leu Leu Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val
                      50
50
     tta ggg cat ccc tta cgg tat atg ctg gag ctg tac cag cgt tca gct
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     Leu Gly His Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala
55
     gac gca agt gga cac cct agg gaa aac cgc acc att ggg gcc acc atg
     531
     Asp Ala Ser Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met
                                                       90
             80
60
     gtg agg ctg gtg agg ccg ctg gct agt gta gca agg cct ctc aga g
     577
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Val	Arg	Leu	Val	Arg	Pro	Leu	Ala	Ser	Val	Ala	Arg	Pro	Leu	Arg
	95			_		100					105			

- gtgagttatc atactatatt gttctggtgg gagggggga gaaaatgggg aagaaagtg 637
 - tagaaaaaag tggatctgtc agttttctgt caggcttcac attgcctnca gtttgtactg 697
- 10 agcaggtctg ttagagagac taaggctagg atataagaag ctaacgcttt gctcttgttc 757
- cctcttacta atgcag gc tcc tgg cac ata cag acc ctg gac ttt cct ctg 808
- Gly Ser Trp His Ile Gln Thr Leu Asp Phe Pro Leu
 110 115 120
 - aga cca aac cgg gta gca tac caa cta gtc aga gcc act gtg gtt tac 856
- 20 Arg Pro Asn Arg Val Ala Tyr Gln Leu Val Arg Ala Thr Val Val Tyr
 125 130 135
 - cgc cat cag ctt cac cta act cat tcc cac ctc tcc tgc cat gtg gag
- 25 Arg His Gln Leu His Leu Thr His Ser His Leu Ser Cys His Val Glu 140 145 150
 - ccc tgg gtc cag aaa agc cca acc aat cac ttt cct tct tca gga aga 952
- Pro Trp Val Gln Lys Ser Pro Thr Asn His Phe Pro Ser Ser Gly Arg
 155 160 165
- ggc tcc tca aag cct tcc ctg ttg ccc aaa act tgg aca gag atg gat 1000

 Gly Ser Ser Lys Pro Ser Leu Leu Pro Lys Thr Trp Thr Glu Met Asp 170

 175

 180
 - atc atg gaa cat gtt ggg caa aag ctc tgg aat cac aag ggg cgc agg 1048
- Ile Met Glu His Val Gly Gln Lys Leu Trp Asn His Lys Gly Arg Arg 185 190 195 200
- gtt cta cga ctc cgc ttc gtg tgt cag cag cca aga ggt agt gag gtt
 1096
- Val Leu Arg Leu Arg Phe Val Cys Gln Gln Pro Arg Gly Ser Glu Val 205 210 215
 - ctt gag ttc tgg tgg cat ggc act tca tca ttg gac act gtc ttc ttg 1144
- Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu Asp Thr Val Phe Leu 220 225 230
 - tta ctg tat ttc aat gac act tagagtgttc agaagaccaa acctctccct 1195
- Leu Leu Tyr Phe Asn Asp Thr 235
 - aaaggcctga aagagtttac agaaaaagac ccttctcttc tcttgaggag ggctcgtcaa 1255
- gcaggcagta ttgcatcgga agttcctggc ccctccaggg agcatgatgg gcctgaaagt
 1315

- 15 aaccagtgtt ccctccaccc ttttcaagtc agcttccagc agctgggctg ggatcactgg 1375 atcattgctc cccatctcta taccccaaac tactgtaagg gagtatgtcc tcgggtacta 5 1435 cactatggtc tcaattctcc caatcatgcc atcatccaga accttgtcag tgagctggtg 1495 gatcagaatg tccctcagcc ttcctgtgtc ccttataagt atgttcccat tagcatcctt 10 1555 ctgattgagg caaatgggag tatcttgtac aaggagtatg agggtatgat tgcccagtcc 1615
- 15 tgcacatgca ggtgacggca aaggtgcagc tagctcaggt ttcccaagaa 1665
- <210> 8: protein GDF-9B [S1] full 20 <211> 239 <212> PRT <213> Ovis aries <221> misc_feature 25 <222> (253)...(255) <223> atg start codon. <221> misc_feature <222> (1253)..(1255) <223> position of first codon of mature peptide in wildtype sheep. 30 <221> misc feature <222> (685)..() <223> n represents approx 5.2 kb of intron. <221> misc feature $\langle 222 \rangle$ $(162\overline{8})...(1630)$
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 - Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln Pro Ser Ile 30 25 20
 - Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln Glu Leu Leu 45 40 35
- 50 Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val Leu Gly His 60 55 50
- Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala Asp Ala Ser 55 80 75 70 65
- Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met Val Arg Leu 60 90 85

60

								1	6								
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15	Ser Hi 145	s Leu	Ser	Cys	His 150	Val	Glu	Pro	Trp	Val 155	Gln	Lys	Ser	Pro	Thr 160		
	Asn Hi	s Phe	Pro	Ser 165	Ser	Gly	Arg	Gly	Ser 170	Ser	Lys	Pro	Ser	Leu 175	Leu		
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25	Leu Ti	rp Asr 195		Lys	Gly	Arg	Arg 200		Leu	Arg	Leu	Arg 205	Phe	Val	Cys		
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Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly Leu Val Leu 1 5 10 15



	ttt 96	atg	gaa	cat	agg	gtc	caa	atg	aca	cag	gta	ggg	cag	ccc	tct	att
	Phe	Met	Glu	His 20	Arg	Val	Gln	Met	Thr 25	Gln	Val	Gly	Gln	Pro 30	Ser	Ile
5	gcc	cac	ctg	cct	gag	gcc	cct	acc	ttg	ccc	ctg	att	cag	gag	ctg	cta
	144 Ala	His		Pro	Glu	Ala	Pro	Thr	Leu	Pro	Leu	Ile	Gln 45	Glu	Leu	Leu
10			35					40						+ + - -	~~~	ant
	192							cag								
45	Glu	Glu 50	Ala	Pro	Gly	Lys	Gln 55	Gln	Arg	Lys	Pro	Arg 60	Val	Leu	GTĀ	HIS
15	CCC 240	tta	cgg	tat	atg	ctg	gag	ctg	tac	cag	cgt	tca	gct	gac	gca	agt
20	Pro 65	Leu	Arg	Tyr	Met	Leu 70	Glu	Leu	Tyr	Gln	Arg 75	Ser	Ala	Asp	Ala	Ser 80
20	gga 288	cac	cct	agg	gaa	aac	cgc	acc	att	ggg	gcc	acc	atg	gtg	agg	ctg
	Gly	His	Pro	Arg	Glu 85	Asn	Arg	Thr	Ile	Gly 90	Ala	Thr	Met	Val	Arg 95	Leu
25		agg	ccg	ctg	gct	agt	gta	gca	agg	cct	ctc	aga	ggc	tcc	tgg	cac
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30	2+2	cad	200			+++	cct	cta			aac	caa	qta	qca	tac	caa
	384	_														Gln
35			115		-			120					125			
	432	_														cat
	Leu	Val 130		Ala	Thr	Val	Val 135		Arg	His	Gln	Leu 140	His	Leu	Thr	His
40			ctc	tcc	tgc	cat	gtg	gag	ccc	tgg	gtc	cag	aaa	agc	cca	acc
	480 Ser 145	His	Leu	Ser	Cys	His 150		Glu	Pro	Trp	Val 155	Gln	Lys	Ser	Pro	Thr 160
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	528 Asn	His	. Phe	Pro	Ser 165		Gly	Arg	Gly	Ser 170	Ser	Lys	Pro	Ser	Leu 175	Leu
50	CCC		act	tac			rato	gat	ato			cat	att	: ggg	caa	aag
	576	;														Lys
55	PIC	о гъ	5 1111	180		. GIU	i Met	. Asp	185		. 010		, , ,	190)	
			g aat	cac	aag	g ggg	g cgc	agg	gtt	cta	a cga	a ctc	cgc	ttc	gtg	, tgt
	624 Let	ı Trp	Asr 195		s Lys	s Gly	y Arç	200	y Val	l Lei	ı Arç	g Lev	205	y Phe	e Val	. Cys
60	672		g cca	a aga	a ggt	agt	gaç	g gtt	ctt	ga	g tto	tgg	j tg	g cat	ggc	e act

Ö°

- Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr 210 tca tca ttg gac act gtc ttc ttg tta ctg tat ttc aat gac act
- 5 717
 Ser Ser Leu Asp Thr Val Phe Leu Leu Tyr Phe Asn Asp Thr
 225 230 235
- tagagtgttc agaagaccaa acctctccct aaaggcctga aagagtttac agaaaaagac 10 777
 - ccttctcttc tcttgaggag ggctcgtcaa gcaggcagta ttgcatcgga agttcctggc 837
- 15 ccctccaggg agcatgatgg gcctgaaagt aaccagtgtt ccctccaccc ttttcaagtc 897
 - agcttccagc agctgggctg ggatcactgg atcattgctc cccatctcta taccccaaac 957
- 20 tactgtaagg gagtatgtcc tcgggtacta cactatggtc tcaattctcc caatcatgcc 1017
- atcatccaga accttgtcag tgagctggtg gatcagaatg tccctcagcc ttcctgtgtc 1077
 - ccttataagt atgttcccat tagcatcctt ctgattgagg caaatgggag tatcttgtac 1137
- 30 aaggagtatg agggtatgat tgcccagtcc tgcacatgca ggtga 1182
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- **35** <211> 239
 - <212> PRT
 - <213> Ovis areis
 - <221> misc feature
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- 40 <223> atg start codon.
 - <221> misc feature
 - <222> (805)..(807)
 - <223> first codon of mature peptide in wildtype sheep.
 - <221> misc feature
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- Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln Glu Leu Leu 35 40 45
 - Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val Leu Gly His 50 55 60

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	Gly	His	Pro	Arg	Glu 85	Asn	Arg	Thr	Ile	Gly 90	Ala	Thr	Met	Val	Arg 95	Leu	
10 -	Val	Arg	Pro	Leu 100	Ala	Ser	Val	Ala	Arg 105	Pro	Leu	Arg	Gly	Ser 110	Trp	His	
15	Ile	Gln	Thr 115	Leu	Asp	Phe	Pro	Leu 120	Arg	Pro	Asn	Arg	Val 125	Ala	Tyr	Gln	
20	Leu	Val 130	Arg	Ala	Thr	Val	Val 135	Tyr	Arg	His	Gln	Leu 140	His	Leu	Thr	His	
25	Ser 145	His	Leu	Ser	Cys	His 150	Val	Glu	Pro	Trp	Val 155	Gln	Lys	Ser	Pro	Thr 160	
0.2	Asn	His	Phe	Pro	Ser 165	Ser	Gly	Arg	Gly	Ser 170	Ser	Lys	Pro	Ser	Leu 175	Leu	
30	Pro	Lys	Thr	Trp 180	Thr	Glu	Met	Asp	Ile 185	Met	Glu	His	Val	Gly 190	Gln	Lys	
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60	aga 48		agt													ttg Leu	

9 6 5

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gac act gtc ttc ttg tta ctg tat ttc aat gac act tagagtgttc
     Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
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     tcttgaggag ggct
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     isoleucine codon
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- ctttcatttt tccttgccct atcctttgtg gtagtggagc ctggatgctg ttacccatgt 180
 - aaaaggaaag gtttaaagcg ttatcctttg ggcttttatc agaacatgtt gctgaacacc 240
- 10 aagcttttca ag atg gtc ctc ctg agc atc ctt aga atc ctt ctt tgg
 288

 Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp
 -265
 -260
- gga ctg gtg ctt ttt atg gaa cat agg gtc caa atg aca cag gta 333
 Gly Leu Val Leu Phe Met Glu His Arg Val Gln Met Thr Gln Val -255
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 Gly Gln Pro Ser Ile Ala His Leu Pro Glu Ala Pro Thr Leu Pro -240 -235 -230
- 25 ctg att cag gag ctg cta gaa gaa gcc cct ggc aag cag cag agg
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 Leu Ile Gln Glu Leu Leu Glu Glu Ala Pro Gly Lys Gln Gln Arg
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- 30 aag ccg cgg gtc tta ggg cat ccc tta cgg tat atg ctg gag ctg
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 Lys Pro Arg Val Leu Gly His Pro Leu Arg Tyr Met Leu Glu Leu
 -210 -205 -200
- 35 tac cag cgt tca gct gac gca agt gga cac cct agg gaa aac cgc 513
 Tyr Gln Arg Ser Ala Asp Ala Ser Gly His Pro Arg Glu Asn Arg -195
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- 40 acc att ggg gcc acc atg gtg agg ctg gtg agg ccg ctg gct agt 558

 Thr Ile Gly Ala Thr Met Val Arg Leu Val Arg Pro Leu Ala Ser -180

 -175

 -170
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 Val Ala Arg Pro Leu Arg
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- caggetteae attgeetnea gtttgtaetg ageaggtetg ttagagagae taaggetagg
 727
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 - atataagaag ctaacgcttt gctcttgttc cctcttacta atgcag gc tcc tgg
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 Gly Ser Trp
 -160
- cac ata cag acc ctg gac ttt cct ctg aga cca aac cgg gta gca 826

-140

-30

-20

His Ile Gln Thr Leu Asp Phe Pro Leu Arg Pro Asn Arg Val Ala -150-145-155

22

- tac caa cta gtc aga gcc act gtg gtt tac cgc cat cag ctt cac 5 871 Tyr Gln Leu Val Arg Ala Thr Val Val Tyr Arg His Gln Leu His -135-130
- cta act cat tcc cac ctc tcc tgc cat gtg gag ccc tgg gtc cag 10 916
 - Leu Thr His Ser His Leu Ser Cys His Val Glu Pro Trp Val Gln -115-125 -120
- aaa agc cca acc aat cac ttt cct tct tca gga aga ggc tcc tca 15 961 Thr Asn His Phe Pro Ser Ser Gly Arg Gly Ser Ser Lys Ser Pro -105-100 -110
- aag oot too otg ttg ooc aaa act tgg aca gag atg gat atc atg gaa 20 1009 Lys Pro Ser Leu Leu Pro Lys Thr Trp Thr Glu Met Asp Ile Met Glu -90 -85 -95
- cat gtt ggg caa aag ctc tgg aat cac aag ggg cgc agg gtt cta cga 25 1057 His Val Gly Gln Lys Leu Trp Asn His Lys Gly Arg Arg Val Leu Arg -80-75 -70
- ctc cgc ttc gtg tgt cag cag cca aga ggt agt gag gtt ctt gag ttc 30 1105 Leu Arg Phe Val Cys Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe -60 -55 -65
- tgg tgg cat ggc act tca tca ttg gac act gtc ttc ttg tta ctg tat 35 1153 Trp Trp His Gly Thr Ser Ser Leu Asp Thr Val Phe Leu Leu Tyr -45 -40-35
- tte aat gac act cag agt gtt cag aag acc aaa cct ctc cct aaa ggc 40 1201 Phe Asn Asp Thr Gln Ser Val Gln Lys Thr Lys Pro Leu Pro Lys Gly
- ctg aaa gag ttt aca gaa aaa gac cct tct ctt ctc ttg agg agg gct 45 1249

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- Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser Leu Leu Leu Arg Arg Ala -15-10 cgt caa gca ggc agt att gca tcg gaa gtt cct ggc ccc tcc agg gag
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- cat gat ggg cct gaa agt aac cag tgt tcc ctc cac cct ttt caa gtc 55 1345 His Asp Gly Pro Glu Ser Asn Gln Cys Ser Leu His Pro Phe Gln Val
- age tte cag cag etg gge tgg gat cae tgg ate att get eec cat etc 60 1393
- Ser Phe Gln Gln Leu Gly Trp Asp His Trp Ile Ile Ala Pro His Leu 45 35

	tat acc	cca	aac	tac	tgt	aag	gga	gta	tgt	cct	cgg	gta	cta	cac	tat
	1441 Tyr Thr	Pro 50	Asn	Tyr	Cys	Lys	Gly 55	Val	Cys	Pro	Arg	Val 60	Leu	His	Tyr
5	ggt ctc		tct	CCC	aat	cat	acc	atc	atc	cag	aac	ctt	gtc	agt	gag
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10	65					70					75				
	ctg gtg 1537														
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	1585 Val Pro	Ile	Ile		Leu	Leu	Ile	Glu		Asn	Gly	Ser	Ile		
20				100					105	•		•		110	
•	aag gag 1627														
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			20					_							
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WO 03/102199 PCT/NZ03/00109

5	Ser	Ala	Asp	Ala -190		Gly	His	Pro	Arg -18		u As	sn Ar	g Th		le 180	Gly
	Ala	Thr	Met	Val -175	_	Leu	Val	Arg	Pro		eu Al	a Se	er Va		la 165	Arg
10	Pro	Leu	Arg	Gly -160		Trp	His	Ile	Gln -15		ır Le	eu As	sp Ph		50 L50	Leu
15	Arg	Pro	Asn	Arg -145		Ala	Туг	Gln	Leu -14		al Ar	g Al	a Tł		al 135	Val
20	Tyr	Arg	His	Gln -130		His	Leu	. Thr	His		er Hi	s Le	eu Se		78 L20	His
25	Val	Glu	Pro	Trp -115		Gln	Lys	: Ser	Pro -11		nr As	șn Hi	s Pl		co L05	Ser
20	Ser	Gly	Arg	Gly -100		Ser	Lys	Pro	Ser -95		ı Lev	ı·Pro	b Lys	-9(p Thr
30	Glu	Met	Asp -85	Ile	Met	Glu	His	Val -80	Gly	Gln	Lys	Leu	Trp -75	Asn	His	Lys
35	Gly	Arg -70	Arg	Val	Leu	_	Leu -65	Arg	Phe	Val	Cys	Gln -60	Gln	Pro	Arg	Gly
40	Ser -55	Glu	Val	Leu	Glu	Phe -50	Trp	Trp	His	Gly	Thr -45	Ser	Ser	Leu	Asp	Thr -40
45	Val	Phe	Leu	Leu	Leu -35	Tyr	Phe	Asn		Thr -30	Gln	Ser	Val	Gln	Lys -25	Thr
	Lys	Pro	Leu	Pro -20	Lys	Gly	Leu	_	Glu -15	Phe	Thr	Glu	Lys	Asp -10	Pro	Ser
50	Leu	Leu	Leu -5	Arg	Arg		Arg -1	_	Ala	Gly	Ser	Ile 5	Ala	Ser	Glu	. Val
55	Pro 10	Gly	Pro	Ser	Arg	Glu 15	His	Asp	Gly	Pro	Glu 20	Ser	Asn	Gln	Cys	Ser 25
60	Leu	His	Pro	Phe	Gln 30	Val	Ser	Phe		Gln 35	Leu	Gly	Trp	Asp	His 40	Trp

Ile Ile Ala Pro His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys 45 50 55

- 5 Pro Arg Val Leu His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile 60 65 70
- Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser 75 80 85
- Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu Ile Glu Ala 90 95 100 105
- Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser 110 115 120

Cys Thr Cys Arg 125

25

- <210> 15: GDF-9B [S2] coding
- <211> 1182
- <212> DNA
- <213> Ovis aries
- 30 <221> misc_feature
 - <222> (1)..(3)
 - <223> atg start codon.
 - <221> mutation
 - <222> (1099)..(1101)
- 35 <223> g to to at 1100 of [S2] sheep changes agc serine codon to atc isoleucine codon
 - <221> CDS
 - <222> (1)..(1179)
 - <221> mat_peptide
- 40 <222> (805)..()
 - <221> misc_feature
 - <222> (1180)..(1182)
 - <223> tga stop codon.
- **45** <400> 15

50

- atg gtc ctc ctg agc atc ctt aga atc ctt ctt tgg gga ctg gtg 45
- Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly Leu Val -265 -255
- ctt ttt atg gaa cat agg gtc caa atg aca cag gta ggg cag ccc
- Leu Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln Pro
 -250 -245 -240
 55
 - tct att gcc cac ctg cct gag gcc cct acc ttg ccc ctg att cag
- Ser Ile Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln
 -235 -230 -225
- gag ctg cta gaa gaa gcc cct ggc aag cag cag agg aag ccg cgg
 180
 Glu Leu Leu Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg

9 6 1

26

-210-215-220gtc tta ggg cat ccc tta cgg tat atg ctg gag ctg tac cag cgt 225 5 Val Leu Gly His Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg -195 -200 -205 tca gct gac gca agt gga cac cct agg gaa aac cgc acc att 270 Ser Ala Asp Ala Ser Gly His Pro Arg Glu Asn Arg Thr Ile Gly 10 -185-180 -190gcc acc atg gtg agg ctg gtg agg ccg ctg gct agt gta gca agg 315 Ala Thr Met Val Arg Leu Val Arg Pro Leu Ala Ser Val Ala Arg 15 -175-170cct ctc aga ggc tcc tgg cac ata cag acc ctg gac ttt cct ctg 360 20 Pro Leu Arg Gly Ser Trp His Ile Gln Thr Leu Asp Phe Pro Leu -150-160-155aga cca aac cgg gta gca tac caa cta gtc aga gcc act gtg gtt 405 25 Arg Pro Asn Arg Val Ala Tyr Gln Leu Val Arg Ala Thr Val -135 -140-145tac ege cat cag ett cae eta aet cat tee cae ete tee tge eat 450 30 Tyr Arg His Gln Leu His Leu Thr His Ser His Leu Ser Cys His -125. -120-130gtg gag ccc tgg gtc cag aaa agc cca acc aat cac ttt cct tct 495 35 Val Glu Pro Trp Val Gln Lys Ser Pro Thr Asn His Phe Pro Ser -110-105-115tca gga aga ggc tcc tca aag cct tcc ctg ttg ccc aaa act tgg aca Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu Pro Lys Thr Trp Thr 40 -90 -100 -95 gag atg gat atc atg gaa cat gtt ggg caa aag ctc tgg aat cac aag 45 Glu Met Asp Ile Met Glu His Val Gly Gln Lys Leu Trp Asn His Lys -75 -85 ggg cgc agg gtt cta cga ctc cgc ttc gtg tgt cag cag cca aga ggt 639 Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys Gln Gln Pro Arg Gly 50 -65 -60 -70 agt gag gtt ctt gag ttc tgg tgg cat ggc act tca tca ttg gac act 687 55 Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu Asp Thr -55 -50-45 gtc ttc ttg tta ctg tat ttc aat gac act cag agt gtt cag aag acc 735 60 Val Phe Leu Leu Tyr Phe Asn Asp Thr Gln Ser Val Gln Lys Thr -30 -35



aaa cct ctc cct aaa ggc ctg aaa gag ttt aca gaa aaa gac cct tct 783 Lys Pro Leu Pro Lys Gly Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser -10 -15 · **-20** 5 ctt ctc ttg agg agg gct cgt caa gca ggc agt att gca tcg gaa gtt 831 Leu Leu Leu Arg Arg Ala Arg Gln Ala Gly Ser Ile Ala Ser Glu Val 10 cct ggc ccc tcc agg gag cat gat ggg cct gaa agt aac cag tgt tcc 879 Pro Gly Pro Ser Arg Glu His Asp Gly Pro Glu Ser Asn Gln Cys Ser 25 20 15 15 ctc cac cct ttt caa gtc agc ttc cag cag ctg ggc tgg gat cac tgg Leu His Pro Phe Gln Val Ser Phe Gln Gln Leu Gly Trp Asp His Trp 40 35 30 20 atc att gct ccc cat ctc tat acc cca aac tac tgt aag gga gta tgt 975 Ile Ile Ala Pro His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys 55 45 25 cct cgg gta cta cac tat ggt ctc aat tct ccc aat cat gcc atc atc 1023 Pro Arg Val Leu His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile 70 30 cag aac ctt gtc agt gag ctg gtg gat cag aat gtc cct cag cct tcc 1071 Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser 85 80 75 35 tgt gtc cct tat aag tat gtt ccc att atc atc ctt ctg att gag gca 1119 Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu Ile Glu Ala 105 100 95 90 40 aat ggg agt atc ttg tac aag gag tat gag ggt atg att gcc cag tcc 1167 Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser 120 115 110 45 tgc aca tgc agg tga 1182 Cys Thr Cys Arg 125 50 <210> 16: protein GDF-9B [S2] coding <211> 393 <212> PRT 55 <213> Ovis aries <221> misc feature <222> (1)..(3) <223> atg start codon. <221> misc feature 60 <222> (1180)..(1182) <223> tga stop codon. <400> 16

60

-85

Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly Leu Val -255 -260 -265 5 Leu Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln Pro -240-245-250Ser Ile Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln 10 -225 -230-235Glu Leu Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg -210 15 -215-220Val Leu Gly His Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg -195-200 -20520 Ser Ala Asp Ala Ser Gly His Pro Arg Glu Asn Arg Thr Ile Gly -180-185 -19025 Ala Thr Met Val Arg Leu Val Arg Pro Leu Ala Ser Val Ala Arg -165-170-175Pro Leu Arg Gly Ser Trp His Ile Gln Thr Leu Asp Phe Pro Leu 30 -150 -155 -160Arg Pro Asn Arg Val Ala Tyr Gln Leu Val Arg Ala Thr Val Val 35 -135 -140-145Tyr Arg His Gln Leu His Leu Thr His Ser His Leu Ser Cys His -120-125 -13040 Val Glu Pro Trp Val Gln Lys Ser Pro Thr Asn His Phe Pro Ser -110-115 45 Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu Pro Lys Thr Trp Thr -90 -95-100

Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys Gln Gln Pro Arg Gly
-65 -60

-80

Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu Asp Thr
-55 -40

Glu Met Asp Ile Met Glu His Val Gly Gln Lys Leu Trp Asn His Lys

-75

Val Phe Leu Leu Tyr Phe Asn Asp Thr Gln Ser Val Gln Lys Thr
-35 -30 -25



Lys Pro Leu Pro Lys Gly Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser -15 -10-205 Leu Leu Leu Arg Arg Ala Arg Gln Ala Gly Ser Ile Ala Ser Glu Val -1 1 -5 10 Pro Gly Pro Ser Arg Glu His Asp Gly Pro Glu Ser Asn Gln Cys Ser 20 25 15 10 15 Leu His Pro Phe Gln Val Ser Phe Gln Gln Leu Gly Trp Asp His Trp 35 . 30 Ile Ile Ala Pro His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys 20 50 55 45 Pro Arg Val Leu His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile 65 70 60 25 Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser 80 85 75 30 Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu Ile Glu Ala 105 95 100 90 Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser 35 120 115 110 Cys Thr Cys Arg 40 125 <210> 17: GDF-9B [S2] mutation <211> 168 45 <212> DNA <213> Ovis aries <221> CDS <222> (1)..(168) <221> mutation 50 <222> (85)..(87) <223> q to t at 86 of GDF9B sheep changes agc serine codon to atc isoleucine codon <400> 17 55 gcc atc atc cag aac ctt gtc agt gag ctg gtg gat cag aat gtc cct Ala Ile Ile Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro 15 10 60 cag cct tcc tgt gtc cct tat aag tat gtt ccc att atc atc ctt ctg Gln Pro Ser Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Leu Leu 25 30 20

att gag gca aat ggg agt atc ttg tac aag gag tat gag ggt atg att Ile Glu Ala Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile gcc cag tcc tgc aca tgc agg tga Ala Gln Ser Cys Thr Cys Arg <210> 18: protein GDF-9B [S2] coding <211> 55 <212> PRT <213> Ovis aries <400> 18 Ala Ile Ile Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Leu Leu Ile Glu Ala Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile

Ala Gln Ser Cys Thr Cys Arg